Applicants have amended the specification to insert SEQ ID Nos, as supported in the present specification.

The following statement is provided to meet the requirements of 37 C.F.R. §1.825(a) and 1.825(b).

I hereby state, in accordance with 37 C.F.R. §1.825(a), that the amendments included in the substitute sheets of the sequence listing are believed to be supported in the application as filed and that the substitute sheets of the sequence listing are not believed to include new matter.

I hereby further state, in accordance with 37 C.F.R. §1.825(b), that the attached copy of the computer readable form is the same as the attached substitute paper copy of the sequence listing.

Under U.S. rules, each sequence must be classified in <213> as an "Artificial Sequence", a sequence of "Unknown" origin, or a sequence originating in a particular organism, identified by its scientific name.

Neither the rules nor the MPEP clarify the nature of the relationship which must exist between a listed sequence and an organism for that organism to be identified as the origin of the sequence under <213>.

Hence, counsel may choose to identify a listed sequence as associated with a particular organism even though that sequence does not occur in nature by itself in that organism (it may be, e.g., an epitopic fragment of a naturally occurring protein, or a cDNA of a naturally occurring mRNA, or even a substitution mutant of a naturally occurring sequence).

Hence, the identification of an organism in <213> should not be construed as an admission that the sequence *per se* occurs in nature in said organism.

Similarly, designation of a sequence as "artificial" should not be construed as a representation that the sequence has no association with any organism. For example, a primer or probe may be designated as "artificial" even though it is necessarily complementary to some target sequence, which may occur in nature. Or an "artificial" sequence may be a substitution mutant of a natural sequence, or a chimera of two or more natural sequences, or a cDNA (i.e., intron-free sequence) corresponding to an intron-containing gene, or otherwise a fragment of a natural sequence.

The examiner should be able to judge the relationship of the enumerated sequences to natural sequences by giving full consideration to the specification, the art cited therein, any further art cited in an IDS, and the results of his or her sequence search against a database containing known natural sequences.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached version is captioned "Version with markings to show changes made".

Applicants submit that the present application contains patentable subject matter and therefore urge the examiner to pass the case to issuance.

If the examiner has any questions or comments concerning the above described application, the examiner is urged to contact the undersigned at the phone number below.

Favorable consideration is respectfully solicited.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the specification:

The paragraph beginning at page 28, line 9, has been amended as follows:

The vector is not specifically limited in so far as it can express the protein of the present invention. Examples thereof include pBAD/His, pRSETA, pcDNA2.1, pTrcHis2A, pYES2, pBlueBac4.5, pcDNA3.1 and pSecTag2 manufacture by Invitrogen, pET and pBAC manufactured by Novagen, pGEM manufactured by Promega, pBluescriptII manufactured by Stratagene, pGEX and pUC18/19 manufactured by Pharmacia, PfastBAC1 manufactured by GIBCO and the like. Preferably, a protein expression vector (described in the specification of a patent application entitled "Protein expression vector and its use" and filed by the same applicant on the same day) is used. This expression vector is constructed by using pCRII-TOPO vector described in the Examples hereinafter, or a commercially available expression vector, for example pSecTag2A vector or pSecTag2B vector (Invitrogen) and integrating a secretory signal nucleotide sequence suitable for expression of the protein of the present invention, in the 3' downstream side thereof, a Tag nucleotide sequence, a cleavable nucleotide sequence and a cloning site, into which a nucleotide sequence encoding a target protein can be inserted, in this order. More specifically, it is preferred to use trypsin signal as the secretory signal, a nucleotide sequence encoding polyhistidine as the Tag nucleotide sequence, and a nucleotide sequence encoding an amino acid sequence which is susceptible to

enzyme-specific cleavage, i.e., a nucleotide sequence encoding the amino acid sequence of Asp-Asp-Asp-Asp-Lys (SEQ ID NO:40) (said amino acid sequence is recognized by enterokinase, and the recombinant fusion protein is cleaved at the C-terminus part thereof) as the cleavable nucleotide sequence.

The paragraph beginning at the bottom of page 59, line 19, has been amended as follows:

Amplification was carried out by using the primers having the sequences represented by SEQ ID NOS: 11 and 12 so that the peptide of Leu-Val-His-Gly (SEQ ID NO:41) was present at the C-terminus of the part from trypsin signal to the enterokinase recognition site of pSecTrypHis/neurosin. This was inserted between NheI and HindIII sites of pSecTag2A to construct the plasmid pTrypSig.

IN THE CLAIMS

Claims 20-22, 30, 32-35 and 37 have been amended as follows:

20(Amended). A vector comprising the nucleotide sequence according to claim ~~2~~43.

21(Amended). Transformed cells having the nucleotide sequence according to claim ~~2~~43 in an expressible state.

22(Amended). A process for producing a protein which comprises culturing cells transformed with the nucleotide sequence (aa), (bb), (cc), (gg), (hh), (ii), (jj), (kk), (ll), (yy) or (zz) of claim ~~2~~ 43, and collecting hBSSP6

produced.

30(Amended). An antibody against the protein according to claim ~~1~~42 or a fragment thereof.

32(Amended). A process for producing a monoclonal antibody against the protein according to claim ~~1~~42 or a fragment thereof which comprises administering the protein according to claim ~~1~~42 or a fragment thereof to a warm-blooded animal other than a human being, selecting the animal whose antibody titer is recognized, collecting its spleen or lymph node, fusing the antibody producing cells contained therein with myeloma cells to prepare a monoclonal antibody producing hybridoma.

33(Amended). A method for determining the protein according to claim ~~1~~42 or a fragment thereof in a specimen which is based on immunological binding of an antibody against the protein or a fragment thereof to the protein or a fragment thereof.

34(Amended). A method for determining BSSP6 or a fragment thereof in a specimen which comprises reacting a monoclonal antibody or a polyclonal antibody against the protein (a), (b), (e), (f), (g), (h), (m), (n), (o) or (p) of claim ~~1~~42 or a modified derivative there of or a fragment thereof and a labeled antibody with BSSP6 or a fragment thereof in the specimen to detect a sandwich complex produced.

35(Amended). A method for determining BSSP6 or a fragment thereof in a specimen which comprises reacting a monoclonal antibody or a polyclonal antibody against the protein (a), (b), (e), (f), (g), (h), (m), (n), (o) or (p) of

claim ~~1~~42 or a modified derivative thereof or a fragment thereof with labeled BSSP6 and BSSP6 or a fragment thereof in the specimen competitively to detect an amount of BSSP6 or a fragment thereof in the specimen based on an amount of the labeled BSSP6 reacted with the antibody.

37(Amended). A diagnostic marker for diseases in tissues comprising the protein according to claim ~~1~~42, or a fragment thereof.